

SEQUENCE LISTING

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Lesage, Florian
Fink, Michel
Lazdunski, Michel

<120> FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS

<130> 1201-CIP-DIV-00

<141> 2001-08-24

<150> 09/144,914

<151> 1998-09-01

<150> 08/749,816

<151> 1996-11-15

<150> 60/095,234

<151> 1998-08-04

<150> FR 96/01565

<151> 1996-02-08

<160> 24

<170> PatentIn Ver. 2.0

<210> 1

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<222> (183)..(1190)

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<223> TWIK-1

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Arg His Arg Ser Ala Trp Cys Phe Gly Phe Leu Val Leu Gly Tyr Leu
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Lys Phe Arg Glu Leu Tyr Lys Ile Gly Ile Thr Cys Tyr Leu Leu Leu	
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Glu Leu Lys Lys Phe Arg Lys Met Phe Tyr Val Lys Lys Asp Lys Asp	
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Glu Asp Leu Leu Arg Gln Glu Leu Arg Lys Leu Lys Arg Arg Phe Leu
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Glu Glu His Glu Cys Leu Ser Glu Gln Gln Leu Glu Gln Phe Leu Gly
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ttc acc tac ctg ctg gtg ggc gcc gcg gtc ttc gac gcg ctg gag tgc 218

Phe Thr Tyr Leu Leu Val Gly Ala Ala Val Phe Asp Ala Leu Glu Ser

20 25 30

gag ccc gag ctg atc gag cgg cag cgg ctg gag ctg cgg cag cag gag 266

Glu Pro Glu Leu Ile Glu Arg Gln Arg Leu Glu Leu Arg Gln Gln Glu

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ctg cgg gcg cgc tac aac ctc agc cag ggc ggc tac gag gag ctg gag 314

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ttc gcc ggc tcc ttc tac ttc gcc atc acc gtc atc acc acc atc ggc 410

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Tyr Gly His Ala Ala Pro Ser Thr Asp Gly Gly Lys Val Phe Cys Met

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Phe Tyr Ala Leu Leu Gly Ile Pro Leu Thr Leu Val Met Phe Gln Ser

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Leu Gly Glu Arg Ile Asn Thr Leu Val Arg Tyr Leu Leu His Arg Ala

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aag aag ggg ctg ggc atg cgg cgc gcc gac gtg tcc atg gcc aac atg 602

Lys Lys Gly Leu Gly Met Arg Arg Ala Asp Val Ser Met Ala Asn Met

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gcc gcc ttc tcc cac tac gag cac tgg acc ttc ttc cag gcc tac tac 698

Ala Ala Phe Ser His Tyr Glu His Trp Thr Phe Phe Gln Ala Tyr Tyr

180 185 190

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Gly	His	Ala	Ala	Pro	Ser	Thr	Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe
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Gln Lys Asp Gln	Ala Leu Gln Thr	Gln Pro Gln Tyr	Val Ala Phe Ser			
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Phe Val Tyr Ile	Leu Thr Gly Leu	Thr Val Ile Gly	Ala Phe Leu Asn			
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Asp Ala Glu His	Arg Ala Leu Leu	Thr Arg Asn Gly	Gln Ala Gly Gly			
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Gly Gly Gly Gly	Gly Ser Ala His	Thr Thr Asp Thr	Ala Ser Ser Thr			
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Ala Ala Ala Gly	Gly Gly Gly Phe	Arg Asn Val Tyr	Ala Glu Val Leu			
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Phe	Tyr	Phe	Ala	Ile	Thr	Val	Ile	Thr	Thr	Ile	Gly	Tyr	Gly	His	Ala	
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Ala	Pro	Ser	Thr	Asp	Gly	Gly	Lys	Val	Phe	Cys	Met	Phe	Tyr	Ala	Leu	
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Ser His Pro Cys Leu Cys Ser Gly Thr Gln Arg Ser Ala Ile Ser Ser
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Arg Arg Ser Ser Val
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 35 40 45

Phe Asn Leu Ile Gly Ala Gly Ile Phe Tyr Leu Ala Glu Thr Gln Asn
 50 55 60

Ser Ser Glu Ser Leu Asn Glu Asn Ser Glu Val Ser Lys Cys Leu His
 65 70 75 80

Asn Leu Pro Ile Gly Gly Lys Ile Thr Ala Glu Met Lys Ser Lys Leu
 85 90 95

Gly Lys Cys Leu Thr Lys Ser Ser Arg Ile Asp Gly Phe Gly Lys Ala
 100 105 110

Ile Phe Phe Ser Trp Thr Leu Tyr Ser Thr Val Gly Tyr Gly Ser Leu
 115 120 125

Tyr Pro His Ser Thr Leu Gly Arg Tyr Leu Thr Ile Phe Tyr Ser Leu
 130 135 140

Leu Met Ile Pro Val Phe Ile Ala Phe Lys Phe Glu Phe Gly Thr Phe
 145 150 155 160

Leu Ala His Phe Leu Val Val Val Ser Asn Arg Thr Arg Leu Ala Val
 165 170 175

Lys Lys Ala Tyr Tyr Lys Leu Ser Gln Asn Pro Glu Asn Ala Glu Thr
 180 185 190

Pro Ser Asn Ser Leu Gln His Asp Tyr Leu Ile Phe Leu Ser Ser Leu
 195 200 205

Leu Leu Cys Ser Ile Ser Leu Leu Ser Ser Ser Ala Leu Phe Ser Ser
 210 215 220
 Ile Glu Asn Ile Ser Tyr Leu Ser Ser Val Tyr Phe Gly Ile Ile Thr
 225 230 235 240
 Met Phe Leu Ile Gly Ile Gly Asp Ile Val Pro Thr Asn Leu Val Trp
 245 250 255
 Phe Ser Gly Tyr Cys Met Leu Phe Leu Ile Ser Asp Val Leu Ser Asn
 260 265 270
 Gln Ile Phe Tyr Phe Cys Gln Ala Arg Val Arg Tyr Phe Phe His Ile
 275 280 285
 Leu Ala Arg Lys Ile Leu Leu Leu Arg Glu Glu Asp Asp Gly Phe Gln
 290 295 300
 Leu Glu Thr Thr Val Ser Leu Gln His Ile Pro Ile Ile Asn Ser Gln
 305 310 315 320
 Cys Met Pro Ser Leu Val Leu Asp Cys Glu Lys Glu Glu Leu Asp Asn
 325 330 335
 Asp Glu Lys Leu Ile Ser Ser Leu Thr Ser Thr
 340 345

<210> 7

<211> 383

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: TWIK-1 homolog

<400> 7

Met Thr Val Ser Met Glu Glu Asn Ser Lys Ile Gln Met Leu Ser Ala
 1 5 10 15
 Thr Ser Lys Asp Lys Lys Val Ala Thr Asp Arg Ser Leu Leu Asn Lys
 20 25 30
 Tyr His Leu Gly Pro Leu Ala Leu His Thr Gly Leu Val Leu Ser Cys
 35 40 45
 Val Thr Tyr Ala Leu Gly Gly Ala Tyr Leu Phe Leu Ser Ile Glu His
 50 55 60
 Pro Glu Glu Leu Lys Arg Arg Glu Lys Ala Ile Arg Glu Phe Gln Asp
 65 70 75 80
 Leu Lys Gln Gln Phe Met Gly Asn Ile Thr Ser Gly Ile Glu Asn Ser
 85 90 95
 Glu Gln Ser Ile Glu Ile Tyr Thr Lys Lys Leu Ile Leu Met Leu Glu
 100 105 110
 Asp Ala His Asn Ala His Ala Phe Glu Tyr Phe Phe Leu Asn His Glu
 115 120 125

Lys	Pro	Arg	Leu	Ser	Phe	Ser	Ser	Lys	Pro	Thr	Val	Leu	Ala	Ser	Arg			
			20				25						30					
Val	Glu	Ser	Asp	Ser	Ala	Ile	Asn	Val	Met	Lys	Trp	Lys	Thr	Val	Ser			
			35				40						45					
Thr	Ile	Phe	Leu	Val	Val	Val	Leu	Tyr	Leu	Ile	Ile	Gly	Ala	Ala	Val			
			50				55						60					
Phe	Lys	Ala	Leu	Glu	Gln	Pro	Gln	Glu	Ile	Ser	Gln	Arg	Thr	Thr	Ile			
			65				70						75					
Val	Ile	Gln	Lys	Gln	Thr	Phe	Ile	Ala	Gln	His	Ala	Cys	Val	Asn	Ser			
			85						90						95			
Thr	Glu	Leu	Asp	Glu	Leu	Ile	Gln	Gln	Ile	Val	Ala	Ala	Ile	Asn	Ala			
			100						105						110			
Gly	Ile	Ile	Pro	Leu	Gly	Asn	Ser	Ser	Asn	Gln	Val	Ser	His	Trp	Asp			
			115						120						125			
Leu	Gly	Ser	Ser	Phe	Phe	Phe	Ala	Gly	Thr	Val	Ile	Thr	Thr	Ile	Gly			
			130						135						140			
Phe	Gly	Asn	Ile	Ser	Pro	Arg	Thr	Glu	Gly	Gly	Lys	Ile	Phe	Cys	Ile			
			145						150						155			
Ile	Tyr	Ala	Leu	Leu	Gly	Ile	Pro	Leu	Glu	Gly	Phe	Leu	Leu	Ala	Gly			
			165						170						175			
Val	Gly	Asp	Gln	Leu	Gly	Thr	Ile	Phe	Gly	Lys	Gly	Ile	Ala	Lys	Val			
			180						185						190			
Glu	Asp	Thr	Phe	Ile	Lys	Trp	Asn	Val	Ser	Gln	Thr	Lys	Ile	Arg	Ile			
			195						200						205			
Ile	Ser	Thr	Ile	Ile	Phe	Ile	Leu	Phe	Gly	Cys	Val	Leu	Phe	Val	Ala			
			210						215						220			
Leu	Pro	Ala	Val	Ile	Phe	Lys	His	Ile	Glu	Gly	Trp	Ser	Ala	Leu	Asp			
			225						230						235			
Ala	Ile	Tyr	Phe	Val	Val	Ile	Thr	Leu	Thr	Thr	Ile	Gly	Phe	Gly	Asp			
			245						250						255			
Tyr	Val	Ala	Gly	Gly	Ser	Asp	Ile	Glu	Tyr	Leu	Asp	Phe	Tyr	Lys	Pro			
			260						265						270			
Val	Val	Trp	Phe	Trp	Ile	Leu	Val	Gly	Leu	Ala	Tyr	Phe	Ala	Ala	Val			
			275						280						285			
Leu	Ser	Met	Ile	Gly	Asp	Trp	Leu	Arg	Val	Ile	Ser	Lys	Lys	Thr	Lys			
			290						295						300			
Glu	Glu	Val	Gly	Glu	Phe	Arg	Ala	His	Ala	Ala	Glu	Trp	Thr	Ala	Asn			
			305						310						315			
Val	Thr	Ala	Glu	Phe	Lys	Glu	Thr	Arg	Arg	Arg	Leu	Ser	Val	Glu	Ile			
			325						330						335			

Tyr Asp Lys Phe Gln Arg Ala Thr Ser Val Lys Arg Lys Leu Ser Ala
340 345 350

Glu Leu Ala Gly Asn His Asn Gln Glu Leu Thr Pro Cys Met Arg Thr
355 360 365

Cys Leu
370

<210> 9
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P1

<400> 9
Phe Thr Ser Ala Leu Phe Phe Ala Ser Thr Val Leu Ser Thr Thr Gly
1 5 10 15

Tyr Gly His Thr Val Pro Leu Ser Asp Gly Gly
20 25

<210> 10
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<223> TWIK-1 P2

<400> 10
Phe Leu Glu Ser Phe Tyr Phe Cys Phe Ile Ser Leu Ser Thr Ile Gly
1 5 10 15

Leu Gly Asp Tyr Val Pro Gly Glu Gly Tyr Asn
20 25

<210> 11
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> TOK-1 P2

<400> 11
Tyr Phe Asn Cys Ile Tyr Phe Cys Phe Leu Cys Leu Leu Thr Ile Gly
1 5 10 15

Tyr Gly Asp Tyr Ala Pro Arg Thr Gly Ala Gly
20 25

<210> 12
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> TOK-1 P1

<400> 12
Tyr Gly Asn Ala Leu Tyr Phe Cys Thr Val Ser Leu Leu Thr Val Gly
1 5 10 15
Leu Gly Asp Ile Leu Pro Lys Ser Val Gly Ala
20 25

<210> 13
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> Slo

<400> 13
Tyr Trp Thr Cys Val Tyr Phe Leu Ile Val Thr Met Ser Thr Val Gly
1 5 10 15
Tyr Gly Asp Val Tyr Cys Glu Thr Val Leu Gly
20 25

<210> 14
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K+ channel sequence

<220>
<223> Shaker

<400> 14
Ile Pro Asp Ala Phe Trp Trp Ala Val Val Thr Met Thr Thr Val Gly
1 5 10 15
Tyr Gly Asp Met Thr Pro Val Gly Phe Trp Gly
20 25

<210> 15
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shab

<400> 15
Ile Pro Glu Ala Phe Trp Trp Ala Gly Ile Thr Met Thr Thr Val Gly
1 5 10 15
Tyr Gly Asp Ile Cys Pro Thr Thr Ala Leu Gly
20 25

<210> 16
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shal

<400> 16
Ile Pro Ala Ala Phe Trp Tyr Thr Ile Val Thr Met Thr Thr Leu Gly
1 5 10 15
Tyr Gly Asp Met Val Pro Glu Thr Ile Ala Gly
20 25

<210> 17
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> Shaw

<400> 17
Ile Pro Leu Gly Leu Trp Trp Ala Leu Val Thr Met Thr Thr Val Gly
1 5 10 15
Tyr Gly Asp Met Ala Pro Lys Thr Tyr Ile Gly
20 25

<210> 18

<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> KAT1

<400> 18
Tyr Val Thr Ala Leu Tyr Trp Ser Ile Thr Thr Leu Thr Thr Thr Gly
1 5 10 15

Tyr Gly Asp Phe His Ala Glu Asn Pro Arg Glu
20 25

<210> 19
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> AKT1

<400> 19
Tyr Val Thr Ser Met Tyr Trp Ser Ile Thr Thr Leu Thr Thr Val Gly
1 5 10 15

Tyr Gly Asp Ile His Pro Val Asn Thr Lys Glu
20 25

<210> 20
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> eag

<400> 20
Tyr Val Thr Ala Leu Tyr Phe Thr Met Thr Cys Met Thr Ser Val Gly
1 5 10 15

Phe Gly Asn Val Ala Ala Glu Thr Asp Asn Glu
20 25

<210> 21
<211> 27

<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> ROMK1

<400> 21
Met Thr Ser Ala Phe Leu Phe Ser Leu Glu Thr Gln Val Thr Ile Gly
1 5 10 15

Tyr Gly Phe Arg Phe Val Thr Glu Gln Cys Ala
20 25

<210> 22
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> IRK1

<400> 22
Phe Thr Ala Ala Phe Leu Phe Ser Ile Glu Thr Gln Thr Thr Ile Gly
1 5 10 15

Tyr Gly Phe Arg Cys Val Thr Asp Glu Cys Pro
20 25

<210> 23
<211> 27
<212> PRT
<213> Unknown

<220>
<223> Description of Unknown Organism: P domain of
representative K⁺ channel sequence

<220>
<223> GIRK1

<400> 23
Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly
1 5 10 15

Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro
20 25

<210> 24
<211> 48
<212> DNA

